

Selection of the fly – Bayesian methods to detect targets of selection in Evolve-and-Resequencing experiments

Experimental evolution studies are powerful approaches to unveil the evolutionary history of lab populations. Such studies have shed light on how selection changes phenotypes and genotypes by being combined with high-throughput sequencing techniques in so-called Evolve-and-Resequencing (E&R) experiments.

We present Bait-ER – a fully Bayesian approach based on the Moran model of allele evolution to estimate selection coefficients from E&R experiments. The model has overlapping generations, a feature that describes several experimental designs found in the literature. We tested our method under several different demographic and experimental conditions to assess its accuracy and precision, and it performs well in most scenarios.

Furthermore, we analyse allele frequency trajectories in *Drosophila pseudoobscura* where we altered their sexual selection regime for 200 generations and sequenced pooled populations at 5 time points. The intensity of sexual selection was either relaxed in monogamous populations (M) or elevated in polyandrous lines (E). We present a comprehensive study of how selection alters population genetics parameters at the chromosome and gene level. We found genomic signatures of adaptation to both regimes in *D. pseudoobscura*. There are more significant variants on E lines as expected from stronger sexual selection. However, we found that the response on the X chromosome was substantial in both treatments, only more marked in E and restricted to chromosome arm XR in M.